Fig. 1

:  $A\beta$  antibody heavy chain variable region : 408 Filename

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Sequence Size : 408 Sequence Position: 1 - 408

								sig	nai	seq	uen	ce							
3.00	10 20 TGGGATGGATCTTTCTC							30			40				— 60				
AI	Jour J	ATC	GA'	CTC	GA'	ICII	TCI	CTI	CCI	CCI	<b>PGTC</b>	AGG	AA(	CTGC	LAG	FTGT	CC	CTC	TGAG
M	G	W	I	W	I	F	L	F	L	L	s	G	T	A	G	V	H	S	E
	70 80 GTCCAGCTGCAGCAGTCTGGACCT							90			1	.00			120				
GT	CCA	GC1	.GC	<b>LGCA</b>	/GT	CTGG	ACC	TGA	GCT	AGI	GAA	GAC	TGO	GGC	TT	CAGT	GAA	GAT	יאיזיאי
V	Q	L	Q	Q	S	G	P	E	L	V	K	T	G	A	S	v	K	I	s
CDR1																			
TG	CAA		.30 'T'T'	чисс	error 2	140		ארוא רו	15	0	- Cmx	1	60	1		170			180 CCAT
ċ	K	A	ŝ	G	Y	S	F	T	.466	TTA	Y	CAT M	H H	W W	iGG:1 V	ICAA K	GCA O	GAG S	
					_	_	-	•	<u> </u>			44			-		_	5	H
																CDR	2		
GG	190 200 GGAAAGAGCCTTGAGTGGAT								21	0		2	20		230				240
G	K	S	L	E	W	I	TGG G	ATI-A							TGC				
•	**		-	E	**	1	G	T.	_I_	<u>s</u>	<u> </u>	<u> Y</u>	N	G	<u>A</u>	T	<u>_S</u>	Y	<u> </u>
	250				260			27	270		280					300			
CA	GAA	GTT	CAA	.GGG	ΦЛ	<b>AGGC</b>	CAC	TTA	TAC	<b>TGT</b>	'AGA	CAC	ATC	CTC	CAG	CAC	AGC	CTA	CATG
Q_	K	F	K	G	_K	A	T	F	T	V	D	T	S	S	S	T	A	Y	M
																	CD	CDR3	
			10			320			33			3	40			350			360
CA	GTT	CAA	CAG	CCT	GAC	LATC	TGA	<b>AGA</b>	CTC	<b>rg</b> c	GGT	CTA	TTA	CTG	TGC	AAG	AGG	GGC	TAAC
Q	F	N	S	L	T	S	E	D	S	A	V	Y	Y	C	A	R	G	A	N
	370				7	380			39	390			400						
TG	GGT	CTT	TGA	CTA	dro	GGG	CCA	AGG	CAC	CAC	ጥርጥ			CTC	CTC	Δ.			

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Fig. 2

: A $\beta$  antibody light chain variable region Filename

Sequence Size : 387

Sequence Position: 1 - 387

							•	sign	al s	equ	enc	е							
	10 20							30 40									<b>—</b> 60		
AT	${\tt ATGGCCTGGACTTCACTTATACTCTCTCTCTCTGGCTCTGGCTCAGGAGCCAGTTCCCAG}$																		
M	A	W	T	S	L	I	L	S	L	L	A	L	С	S	G	A	S	S	Q
	70 80						90				100			110				120	
GCTGTTGTGACTCAGGAATCTGCACTCACCACATCACCTGGTGGAACAGTCATACTCA													CACT						
A	V	V	${f T}$	Q	E	S	A	L	T	T	S	P	G	G	T	V	I	L	T
	CDR1																		
	130 140							15	0		160			170				180	
TG	TGTCGCTCAAGTACTGGGGCTGTTACAACTAGTAACTATGCCAACTGGGTCCAAGAAAA														AAAA				
C	R	S	S	T	G	A	V	T	T	S	N	Y	A	<u>n</u>	W	V	Q	E	K
	CDR2																		
	190				200		210			220				230				240	
CCAGATCATTTATTCACTGGTCTAATAGGTGGTACCAGCAACCGAGCTCCAGGTGTT													TCCT						
P	D	H	L	F	${f T}$	G	L	I	G	G	T	S	N	R	A	<u> P</u>	_ <b>_</b> G	V	P
	250			260				27	70	280				290				300	
GTCAGATTCTCAGGCTCCCTGATTGGAGACAAGGCTGCCCTCACCATCACAGGGGCACAG																			
V	R	F	S	G	S	L	I	G	D	K	A	A	L	T	I	T	G	A	Q
													_						

330

TEDDAMYFC ALWYSTHYV

**ACTGAGGATGATGCAATGTATTTCTGTGCTCTATGGTACAGCACCCATTATGTTTTCGGC** 

340

350

360

370 380 GGTGGAACCAAGGTCACTGTCCTAGGT G G T K V T V L G

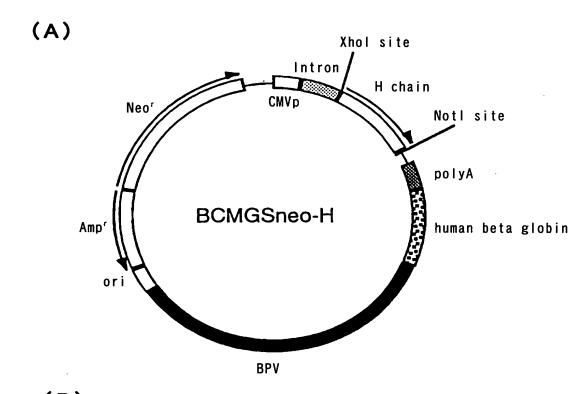
320

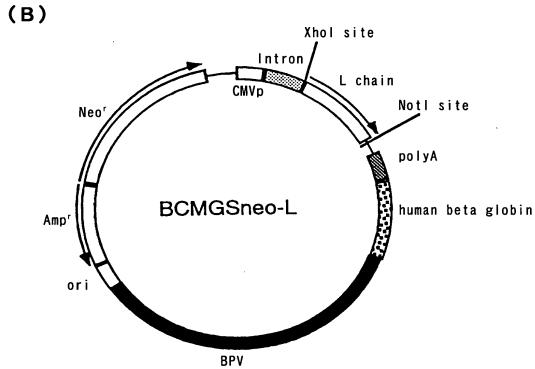
310

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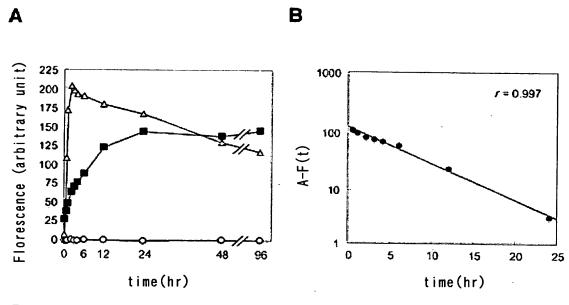
Fig. 3



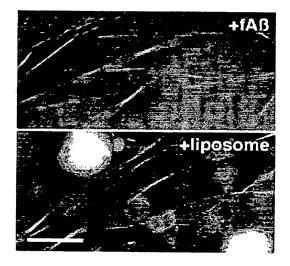


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Fig. 4

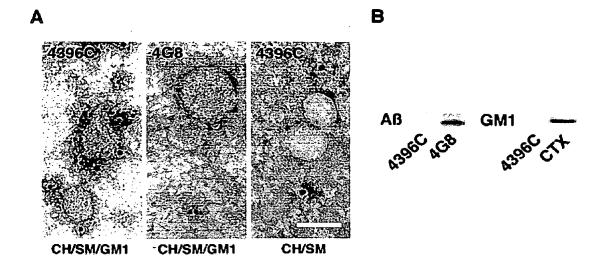


C

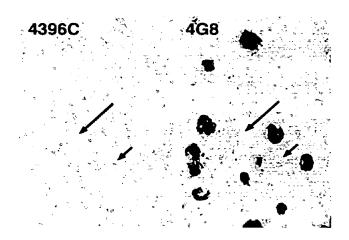


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Fig. 5

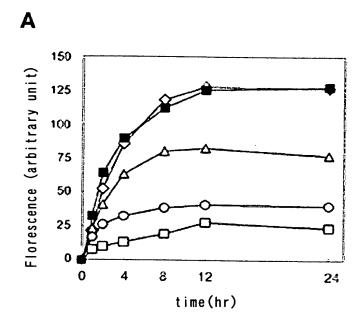


C

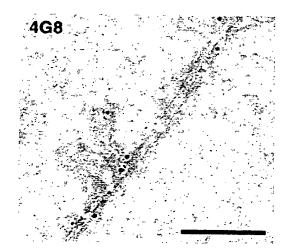


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Fig. 6



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Fig. 7

3'

